Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 03:46:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779428.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1779428 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779428_1.fastq.gz SRR1779428_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 03:46:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779428.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,777,076
Mapped reads	18,076,672 / 91.4%
Unmapped reads	1,700,404 / 8.6%
Mapped paired reads	18,076,672 / 91.4%
Mapped reads, first in pair	9,089,310 / 45.96%
Mapped reads, second in pair	8,987,362 / 45.44%
Mapped reads, both in pair	17,897,480 / 90.5%
Mapped reads, singletons	179,192 / 0.91%
Secondary alignments	0
Supplementary alignments	224,249 / 1.13%
Read min/max/mean length	30 / 80 / 80.41
Duplicated reads (estimated)	11,854,967 / 59.94%
Duplication rate	22.62%
Clipped reads	1,857,455 / 9.39%

2.2. ACGT Content

Number/percentage of A's	417,787,167 / 29.31%
Number/percentage of C's	293,327,504 / 20.58%
Number/percentage of T's	414,862,626 / 29.11%
Number/percentage of G's	299,087,742 / 20.98%
Number/percentage of N's	306,793 / 0.02%

GC Percentage	41.56%

2.3. Coverage

Mean	0.4605
Standard Deviation	130.5232

2.4. Mapping Quality

Mean Mapping Quality	50.67

2.5. Insert size

Mean	128,280.04
Standard Deviation	2,778,152.41
P25/Median/P75	125 / 162 / 209

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	5,791,111
Insertions	235,179
Mapped reads with at least one insertion	1.29%
Deletions	163,416
Mapped reads with at least one deletion	0.9%
Homopolymer indels	35.33%

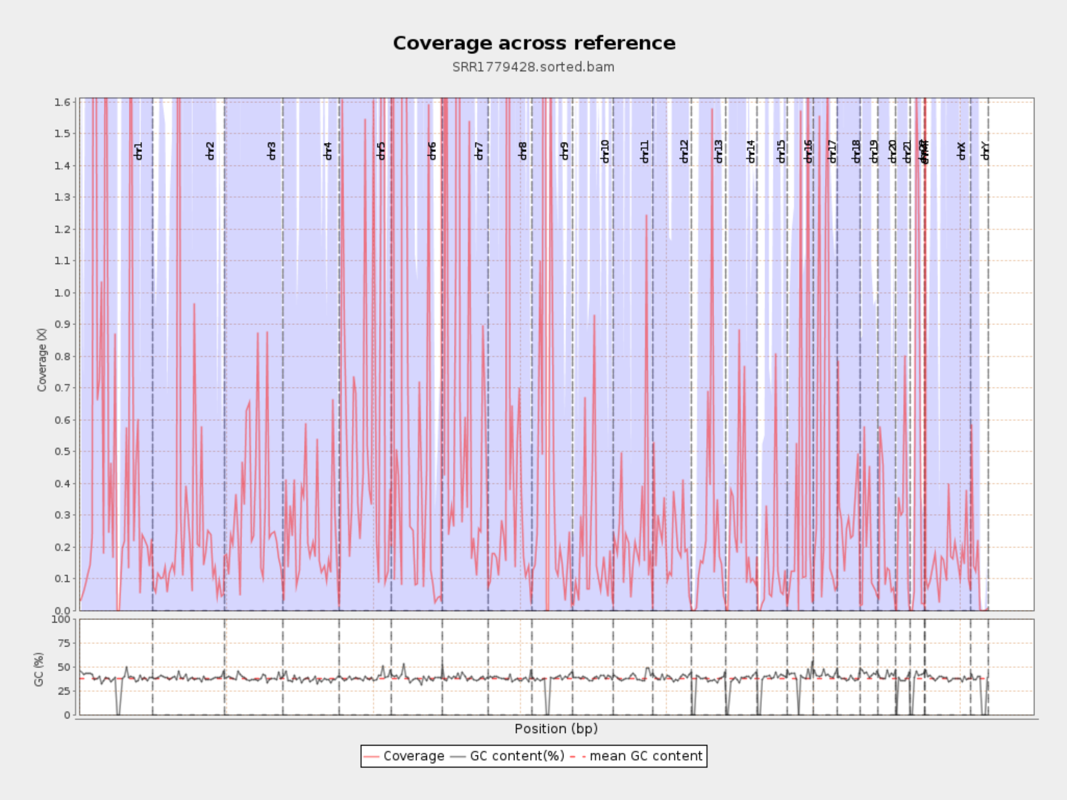
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

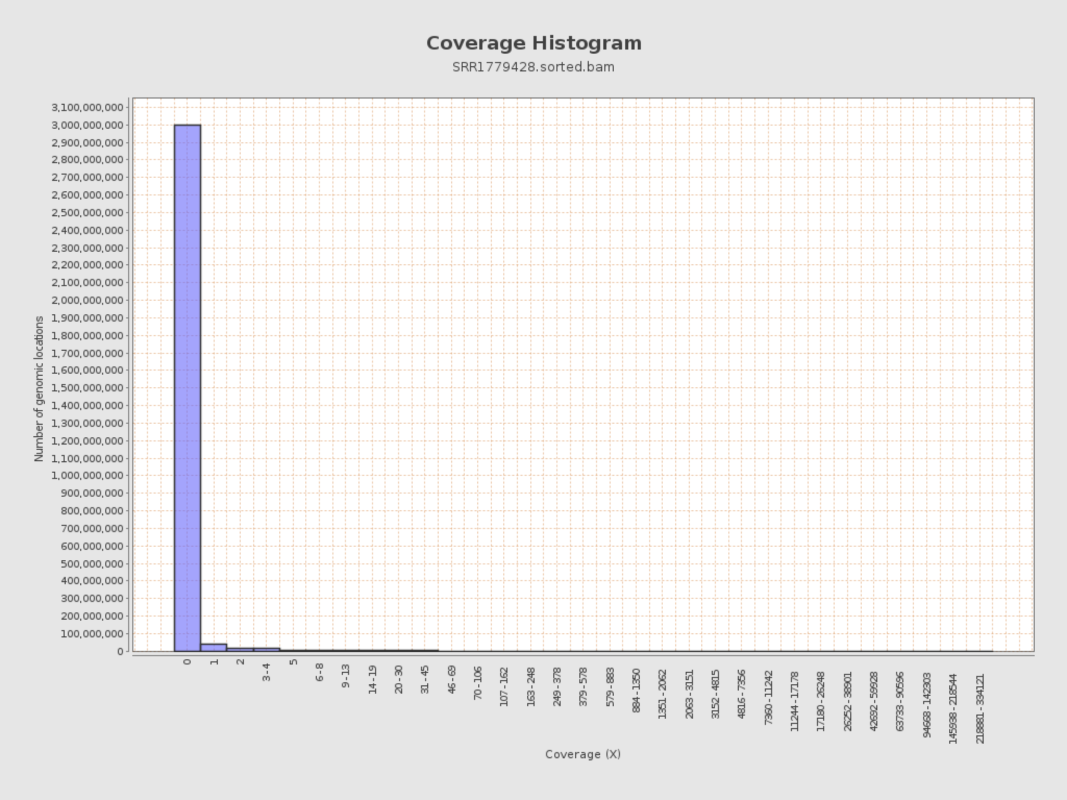
		bases	coverage	deviation
chr1	249250621	129343953	0.5189	44.8996
chr2	243199373	68988690	0.2837	37.4866
chr3	198022430	62042009	0.3133	10.6006
chr4	191154276	48113293	0.2517	9.5277
chr5	180915260	144310530	0.7977	45.9857
chr6	171115067	258141819	1.5086	528.5072
chr7	159138663	205420583	1.2908	107.208
chr8	146364022	69557215	0.4752	70.7155
chr9	141213431	76266967	0.5401	58.0096
chr10	135534747	27930603	0.2061	9.1064
chr11	135006516	35284274	0.2614	15.5694
chr12	133851895	30560127	0.2283	7.6259
chr13	115169878	32118139	0.2789	7.1238
chr14	107349540	27624098	0.2573	6.5604
chr15	102531392	13992357	0.1365	21.0534
chr16	90354753	36245094	0.4011	55.2126
chr17	81195210	42555585	0.5241	38.7738
chr18	78077248	24038554	0.3079	7.3356
chr19	59128983	11542849	0.1952	16.7727
chr20	63025520	11872137	0.1884	3.3536
chr21	48129895	14322661	0.2976	4.9877
chr22	51304566	24004160	0.4679	45.638
chrMT	16571	223391	13.4808	7.384
chrX	155270560	24301171	0.1565	3.3263

chrY	59373566	6866782	0.1157	8.0753

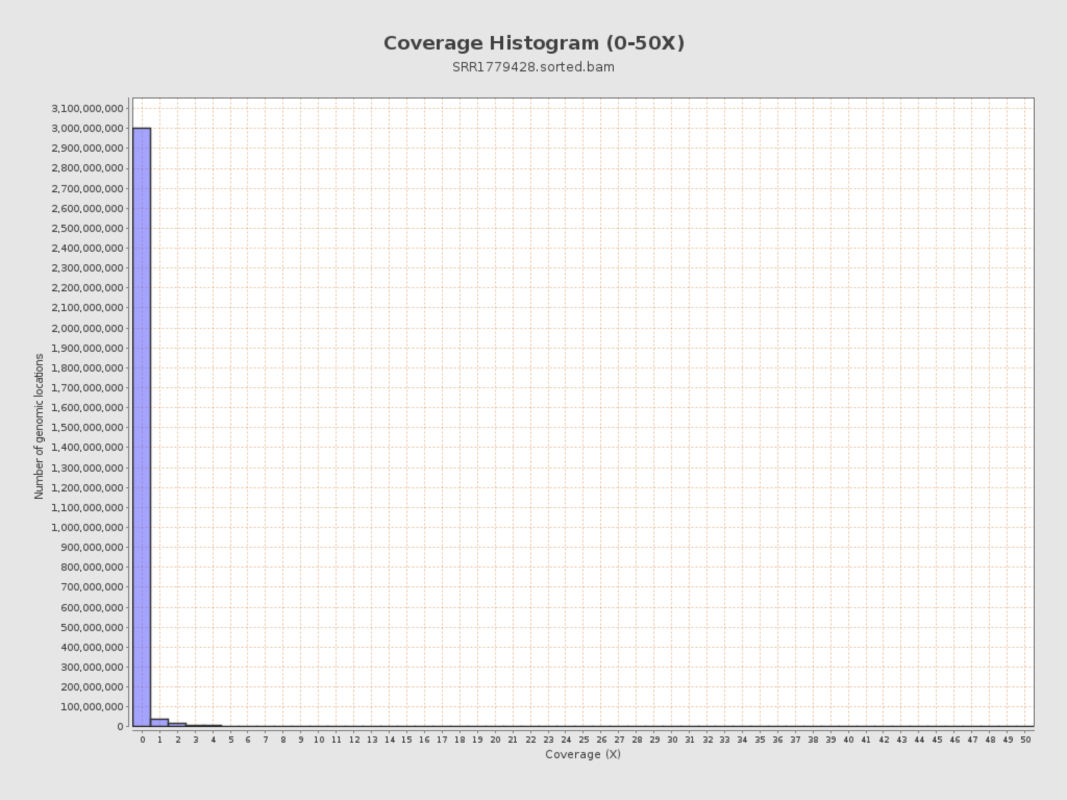
3. Results : Coverage across reference



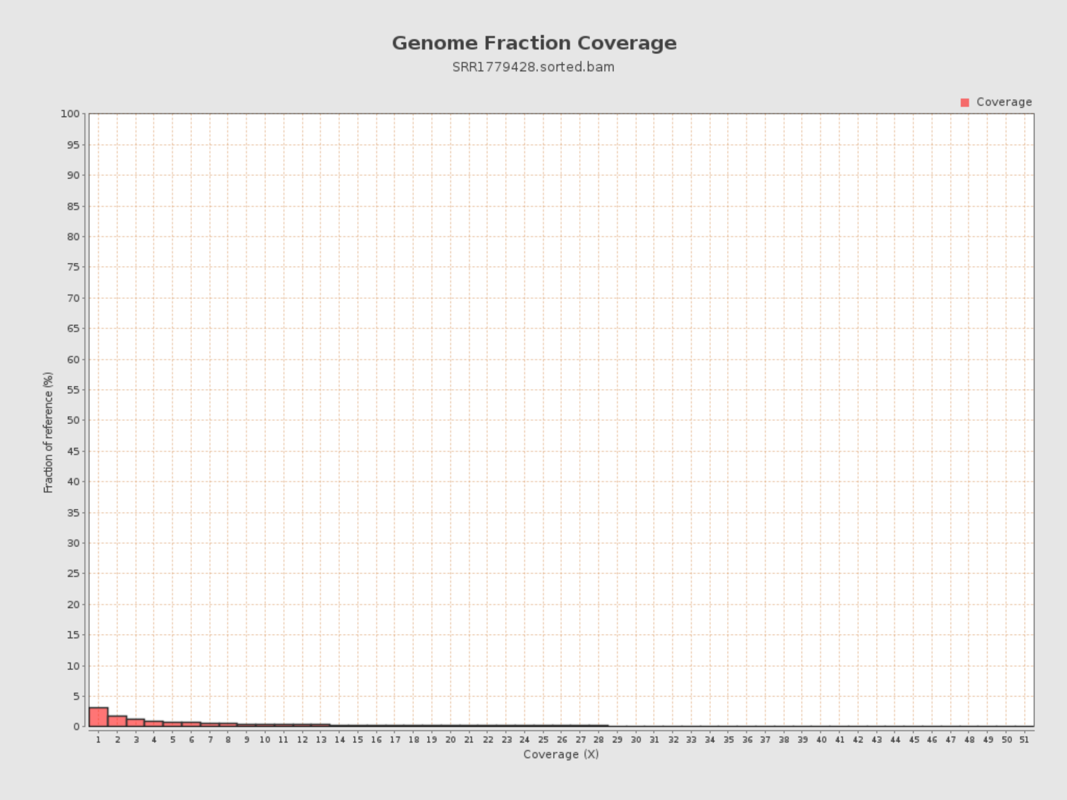
4. Results : Coverage Histogram



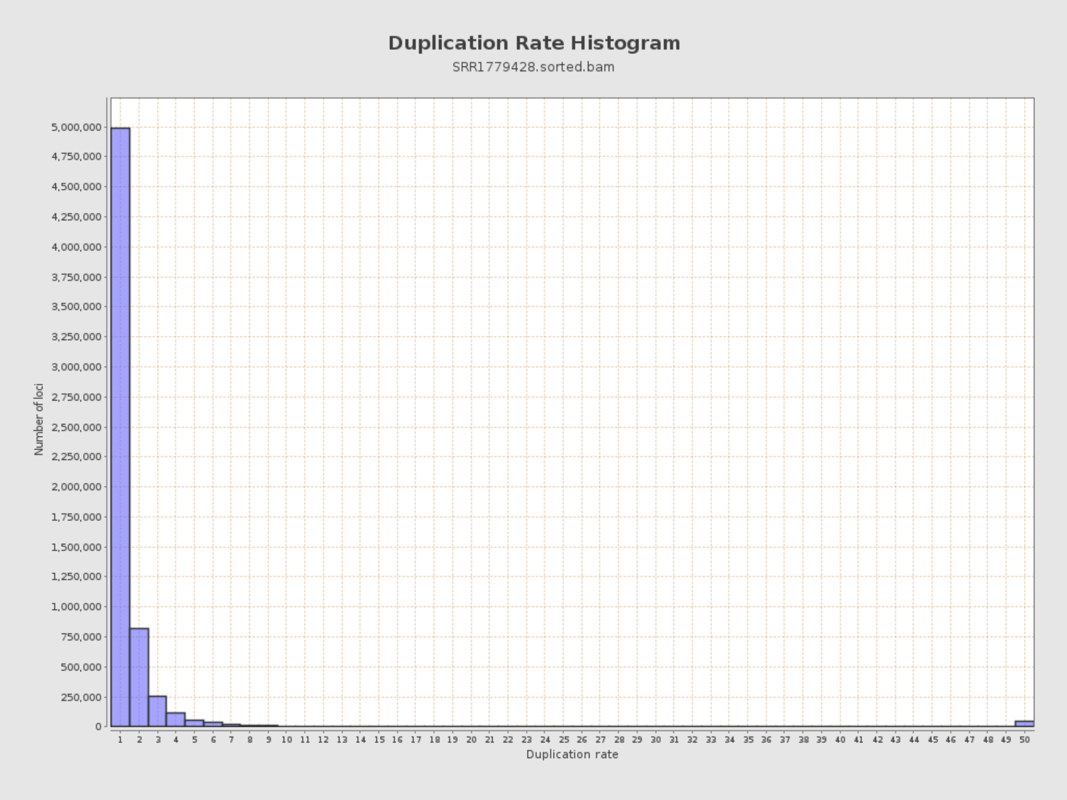
5. Results : Coverage Histogram (0-50X)



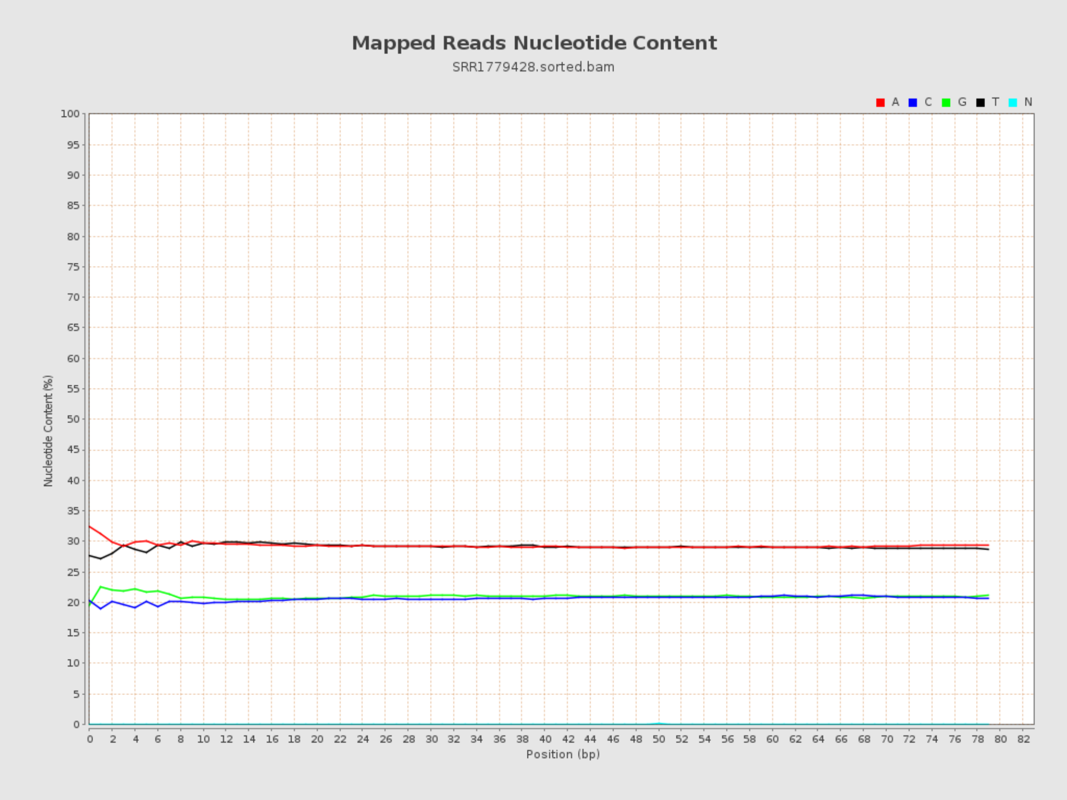
6. Results : Genome Fraction Coverage



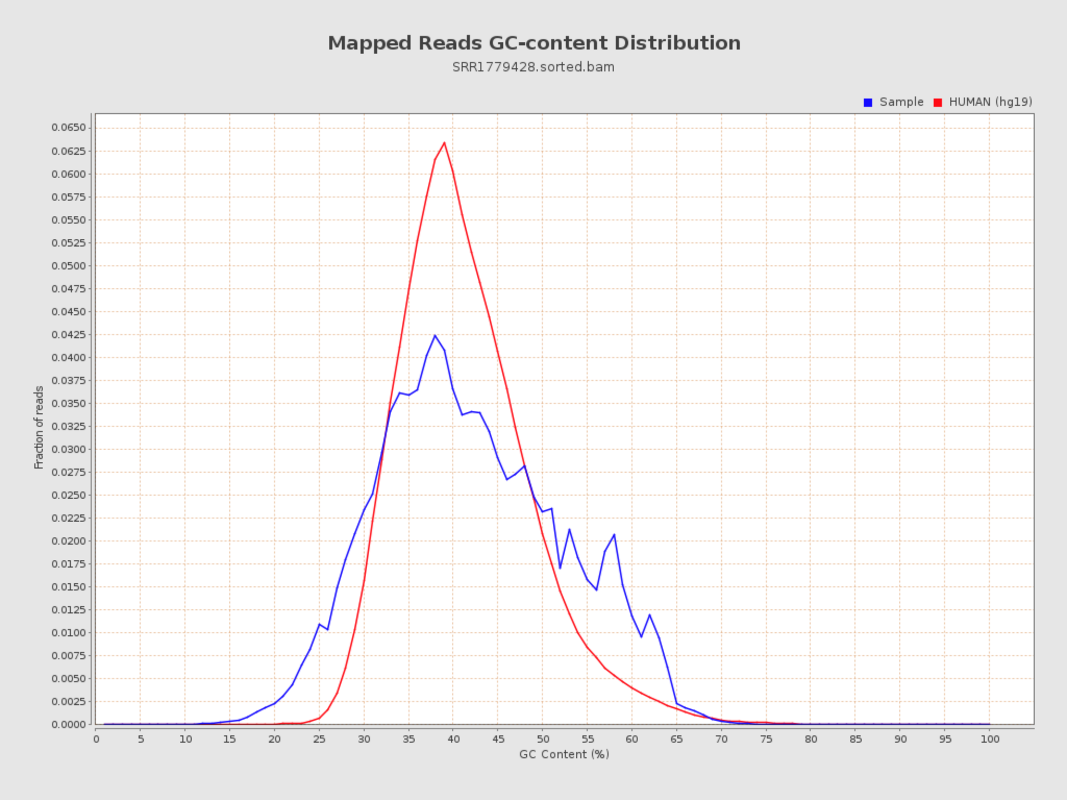
7. Results : Duplication Rate Histogram



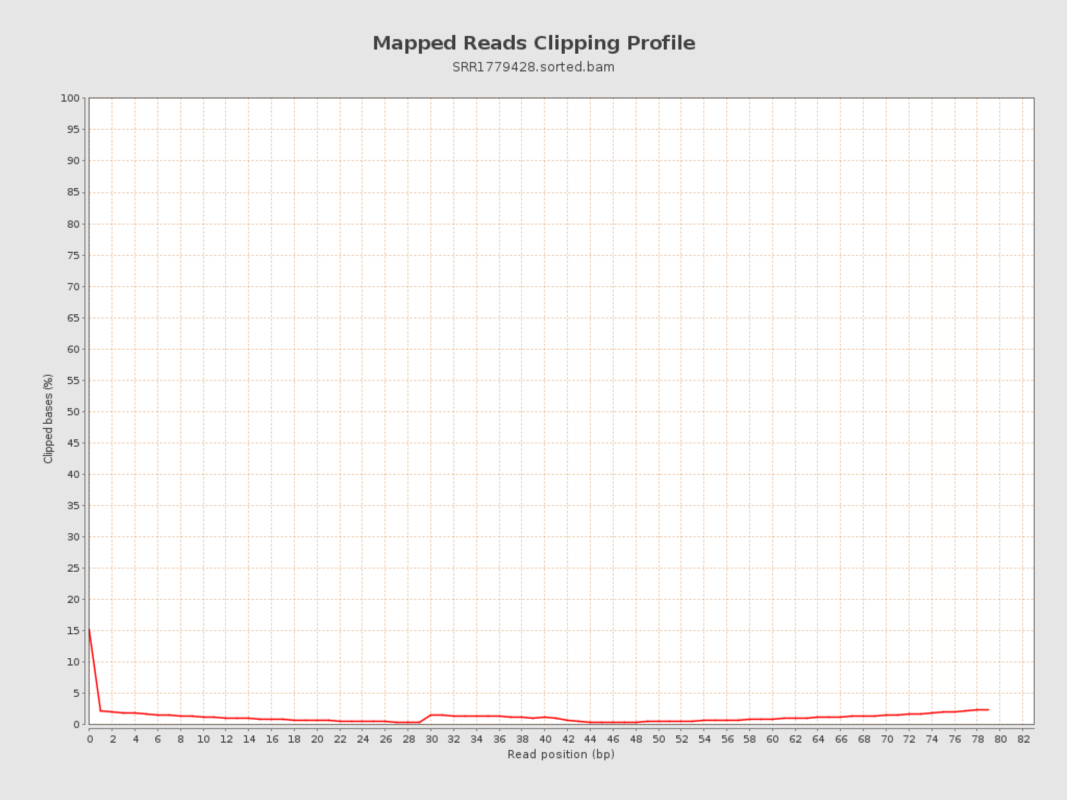
8. Results : Mapped Reads Nucleotide Content



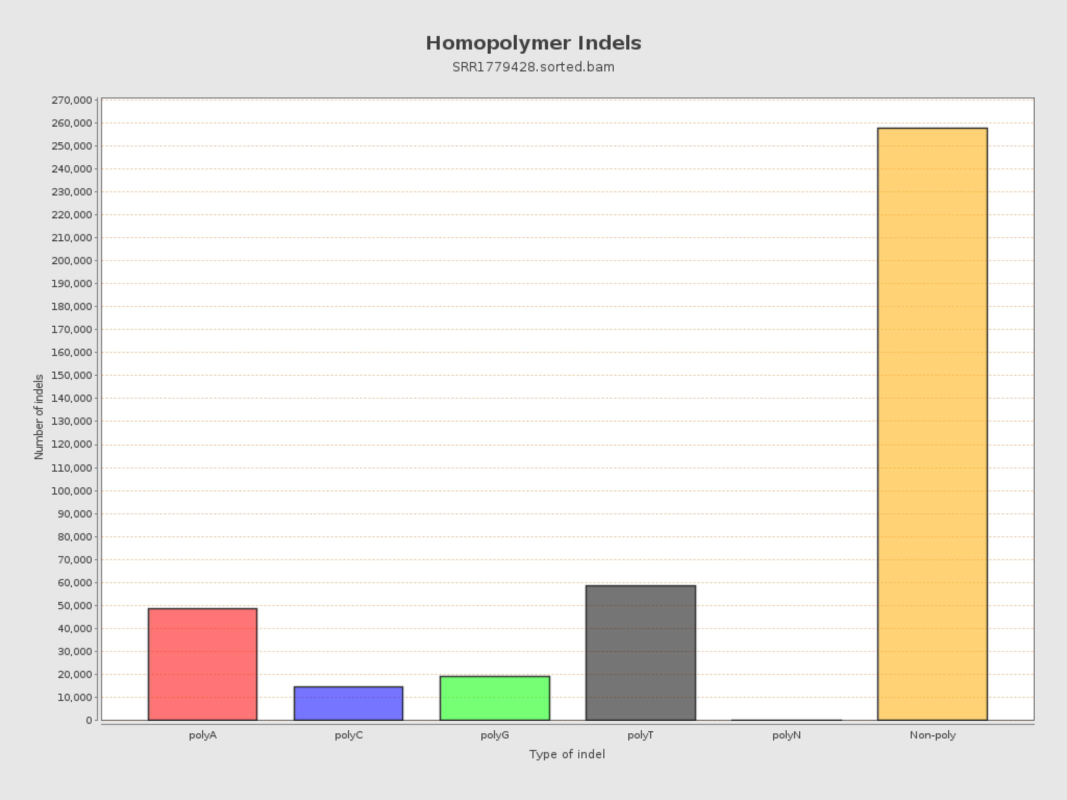
9. Results : Mapped Reads GC-content Distribution



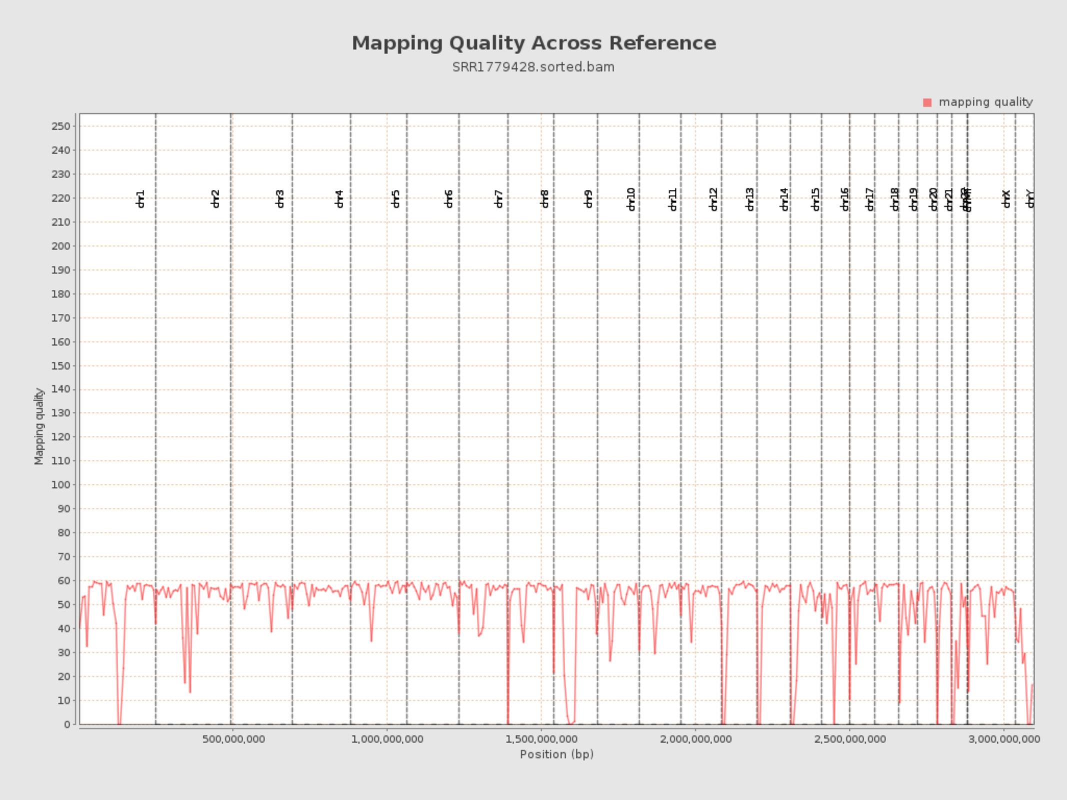
10. Results : Mapped Reads Clipping Profile



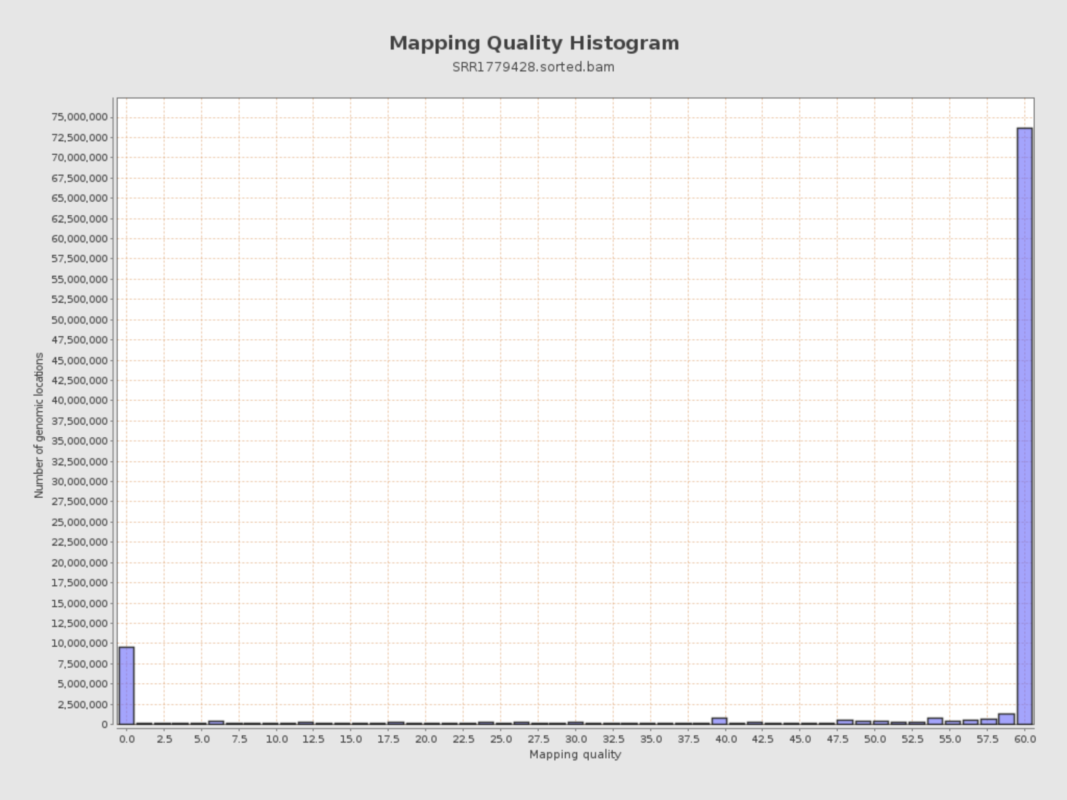
11. Results : Homopolymer Indels



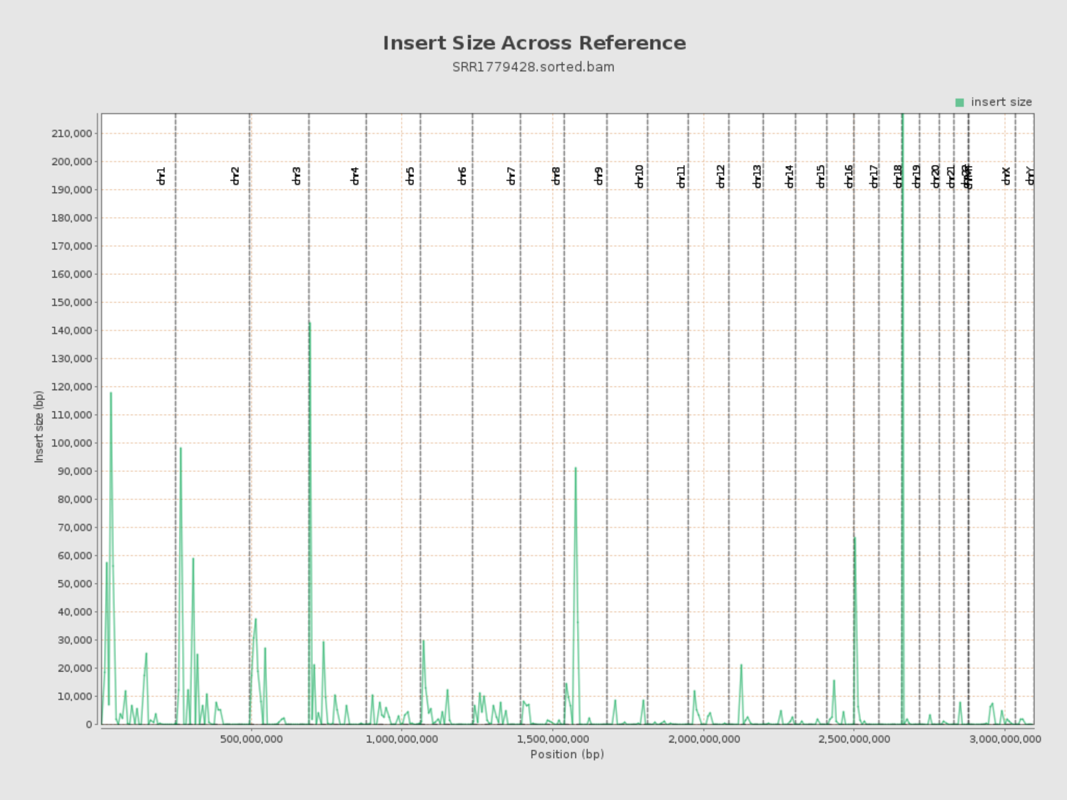
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram